Hydrogen and Bioenergetics in the Yellowstone Geothermal Ecosystem

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The overarching goal of this work is to characterize the driving bioenergetics of geothermal ecosystems. The Yellowstone National Park geothermal ecosystem is generally considered to be supported by sulfur metabolism, but molecular phylogenetic studies of YNP communities indicate, unexpectedly, that hydrogen-metabolizing organisms, both known and novel consortia or communities, may dominate this and other geothermal ecosystems. Hydrogen-metabolizing microorganisms potentially are involved in several geological processes, such as the formation of ore bodies and the erosion of rock in all environments. Yet, little is known about how hydrogen functions in natural microbial communities.

In order to survey the distribution of hydrogen concentrations in high-temperature Yellowstone waters (pools, streams, hydrothermal vents, and a well) we pumped source waters and performed air-bubble-stripping with H_2 analysis by gas chromatography. The results indicate levels from 3 to 300 nM H_2. A molecular phylogenetic survey screened 2000 SSU rRNA gene clones from microbial communities at locations with significant concentrations of hydrogen, to determine the nature and quantities of microbial diversity that constitute these ecosystems. Analyses indicate the ubiquitous dominance by uncultured organisms of the phylogenetic kinds that rely exclusively on H_2 as an energy source. Thermodynamic modeling of field determined hydrogen and geochemical parameters show the preferential electron donor to be hydrogen. The results indicate that a molecular phylogenetic survey can predict the underlying bioenergetics of a microbial ecosystem. Collectively, the results indicate that H_2 rather than sulfur metabolism, is the dominate metabolism in this and potentially other geo- hydro- thermal ecosystems.